

**Molecular Signatures of Life  
in the Dead Sea**  
A DDF Initiative

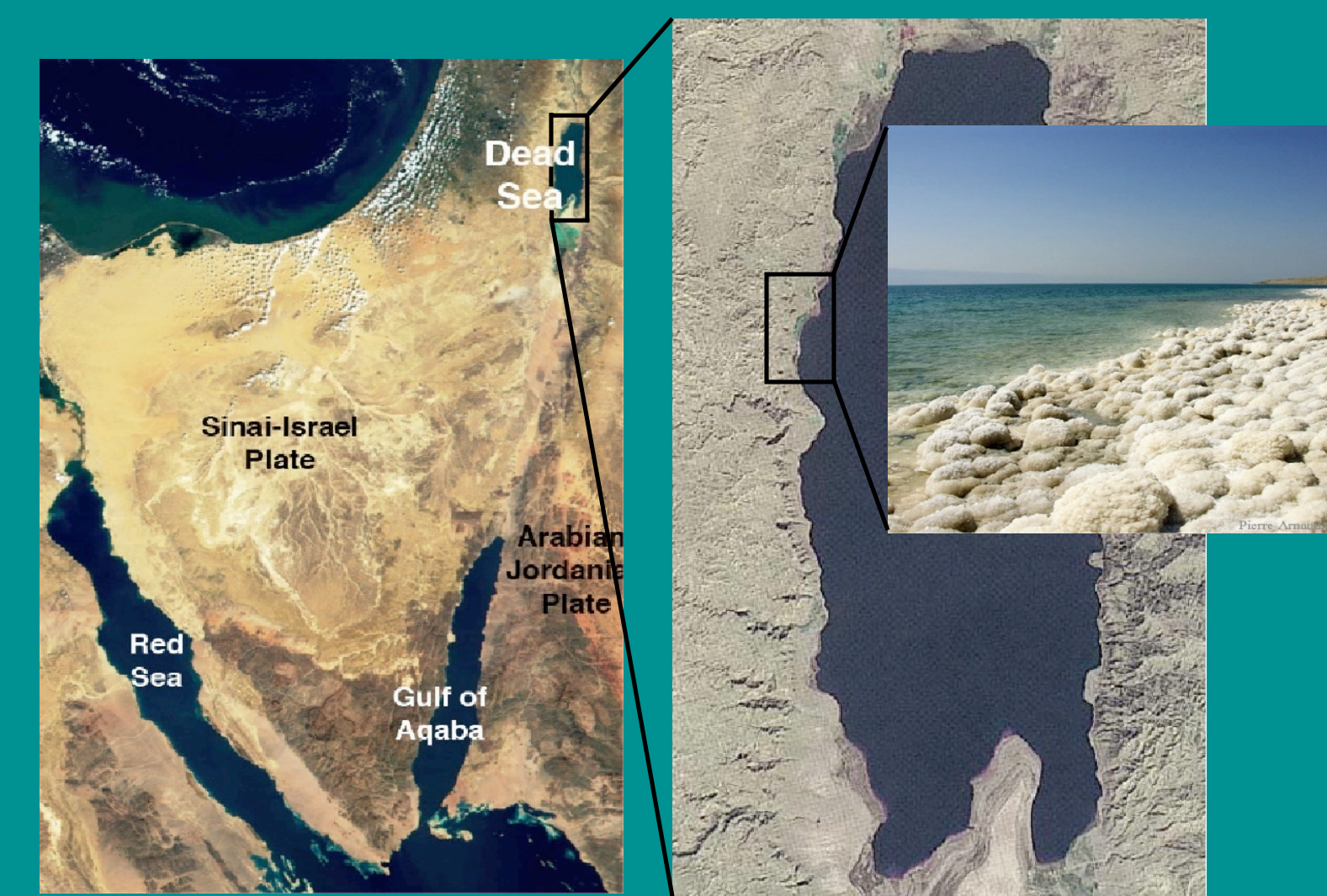


Matthew Rhodes  
and  
Chris House



NASA NAI Update  
08/14/08

## The Dead Sea



## The Dead Sea as a Mars analog



Holden Crater

1. Tectonic basin ~ -418m
2. Salinity ~ 340‰
3. Acidic pH ~ 6



Matthew Rhodes



Valle Marineris

## Objectives

**Comprehensively characterize life in a unique hypersaline environment:**

1. Cellular signatures (SIMS)
2. Lipid signatures (lipids)
3. Amino acid signatures
4. DNA signatures (metagenomics)

## Cellular Signatures

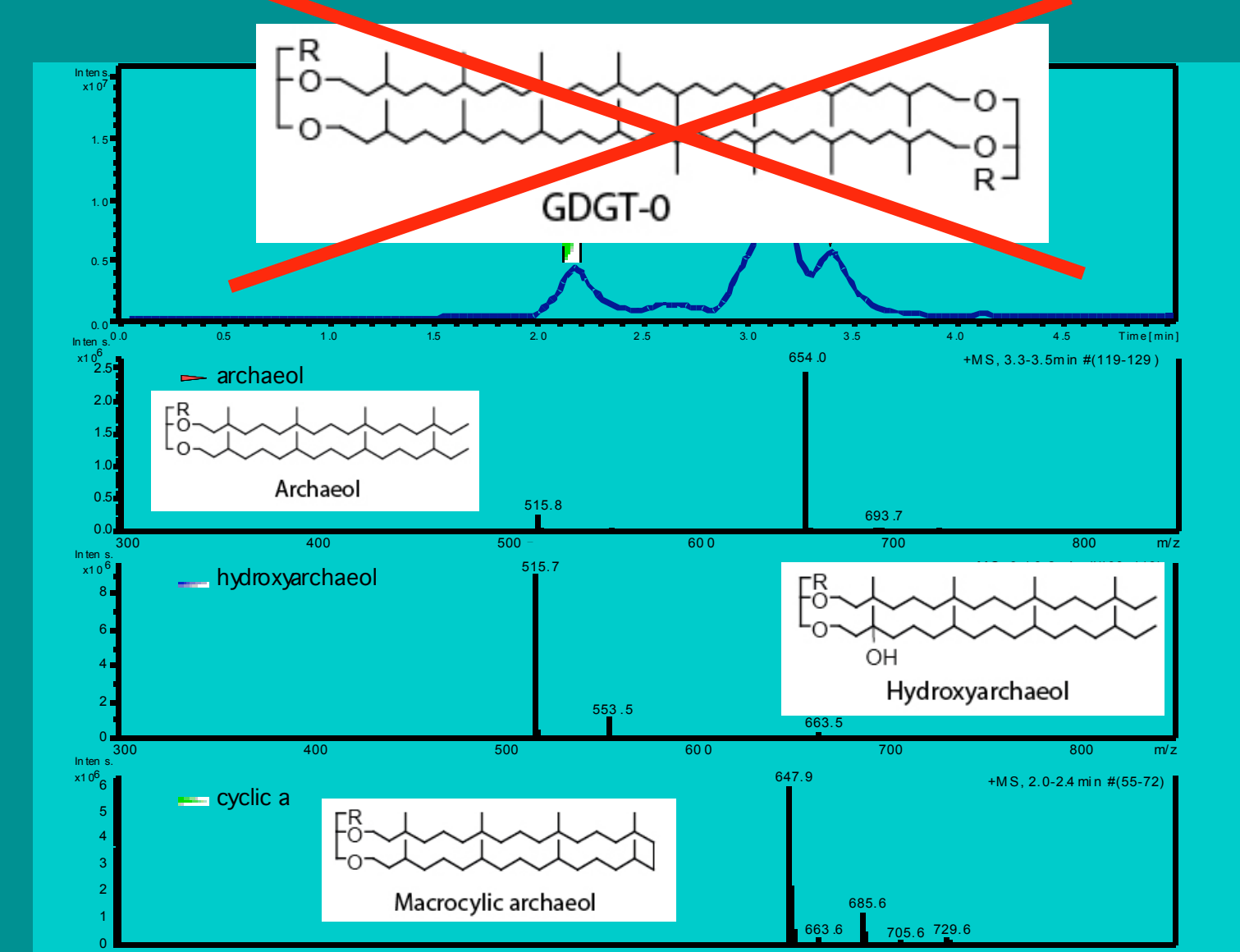
SIMS to monitor uptake of isotopically  
labeled carbon and nitrogen  
→Reveal which organisms are primary  
producers

Incubations  
conducted in  
the field



# Initial Results Lipids

## Initial Results Lipids

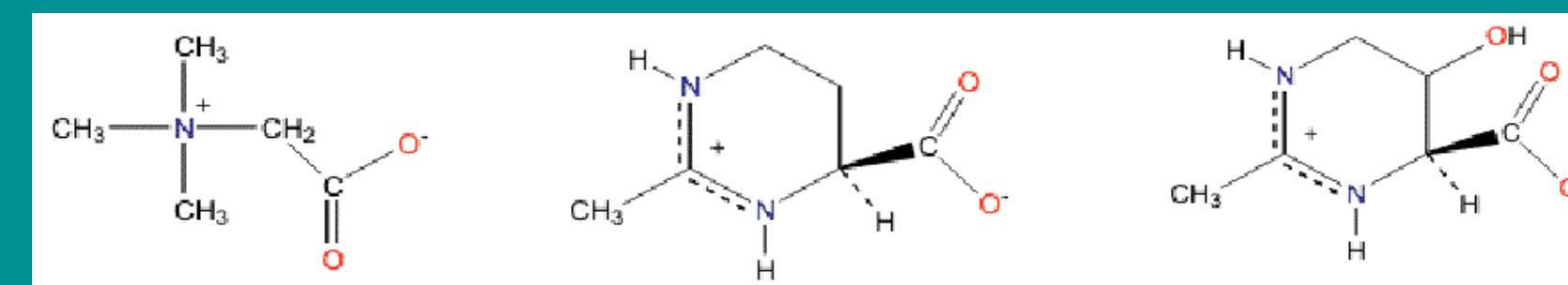


## Amino Acid Analysis Intro

- Two high salinity coping mechanisms
  1. Organic in
    - Energetically expensive
    - Does not require protein alteration
  2. Salt in
    - Energetically Cheap
    - Requires protein alteration
    - ↑ Acidic AAs   ↓ Basic AAs   Low hydrophobic AAs
    - Salt in more prevalent at higher salinities

## Amino Acid Signatures

1. Degree of racemization  
→Reveal level of microbial activity
2. Presence of unusual amino acids  
Betaine, Ectoine, and hydroxectoine used by halophiles as osmolytes

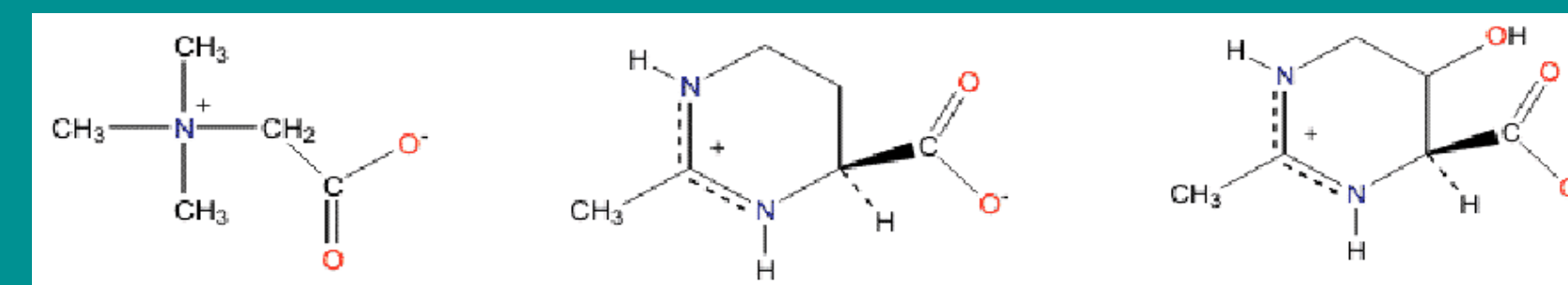


Samples run  
Awaiting analysis

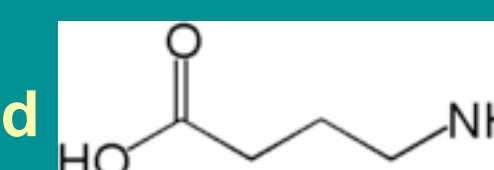
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$\gamma$ -aminobutyric acid



PESS STATE

PESS STATE

## DNA Signatures

### “Pyrosequencing” of the Dead Sea

- Novel sequencing method
- Massively parallel (~400,000 sequences per plate)\*
- Yields very short reads (~200 bp)
- PSU is a good place to do this work

- As examples,  
our modern Dead Sea half-plate gave 273,296 sequences with an average read length of 251 bp,  
  
and last week, we had a full plate yield 546,127 reads with an average length of ~194 bp (105 Mb).

454 Sequencing  
(to compare today's Dead Sea  
with the 1992 bloom event)

1. 16S rRNA sequence tags to look at  
species distribution
2. Non-specific DNA sequencing  
(2x400,000)
3. Assembled fosmid sequences

End up with close to ~200 Mb of data

## Sequencing Status

1. Amplicons ready for sequencing

2. Fosmids:

1 complete 40kb fosmid

Majority of ORFs are haloarchaeal

However, bacterial ORF every so often

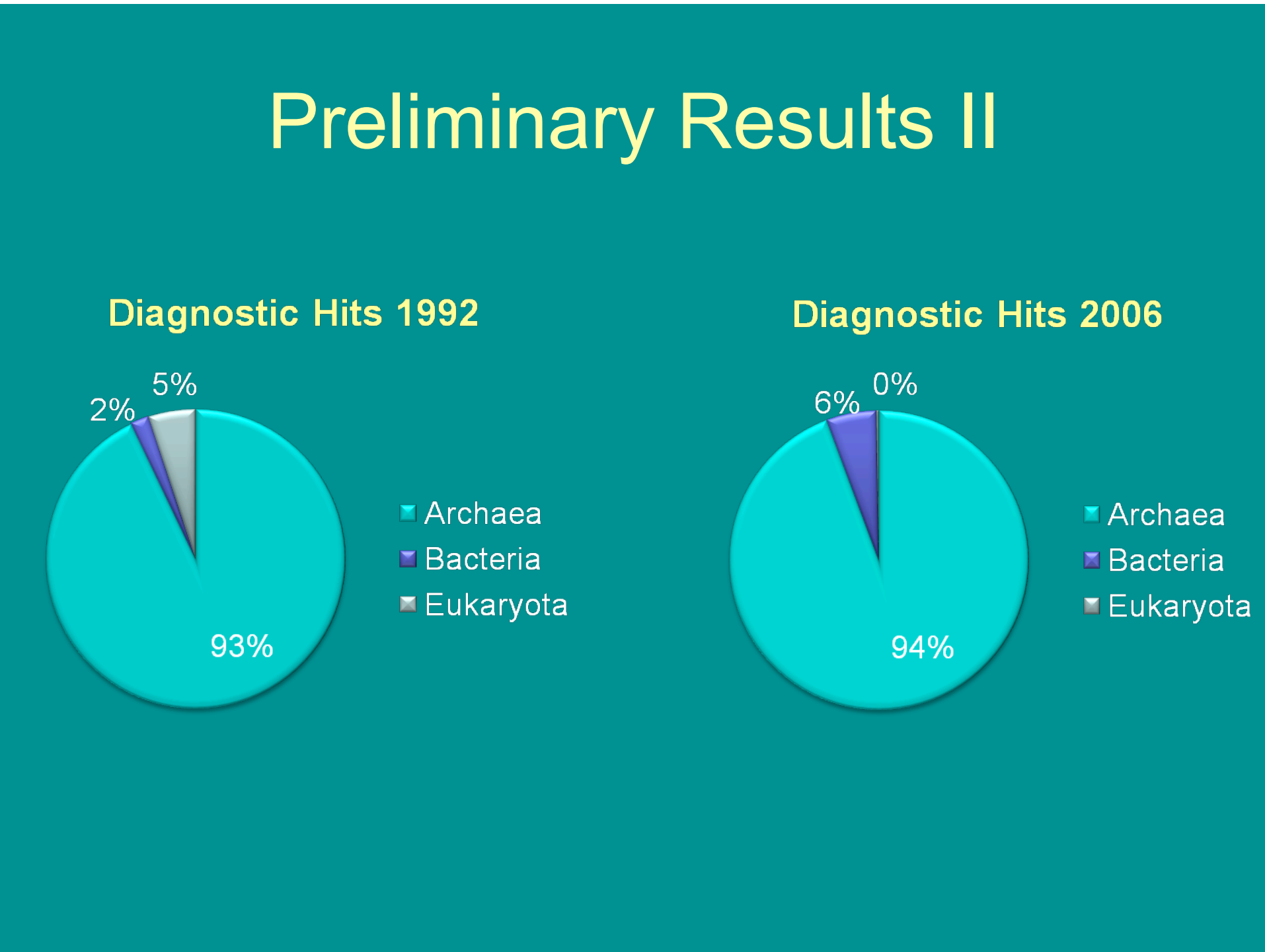
(e.g., citryl-CoA lyase from  
an actinobacteria)

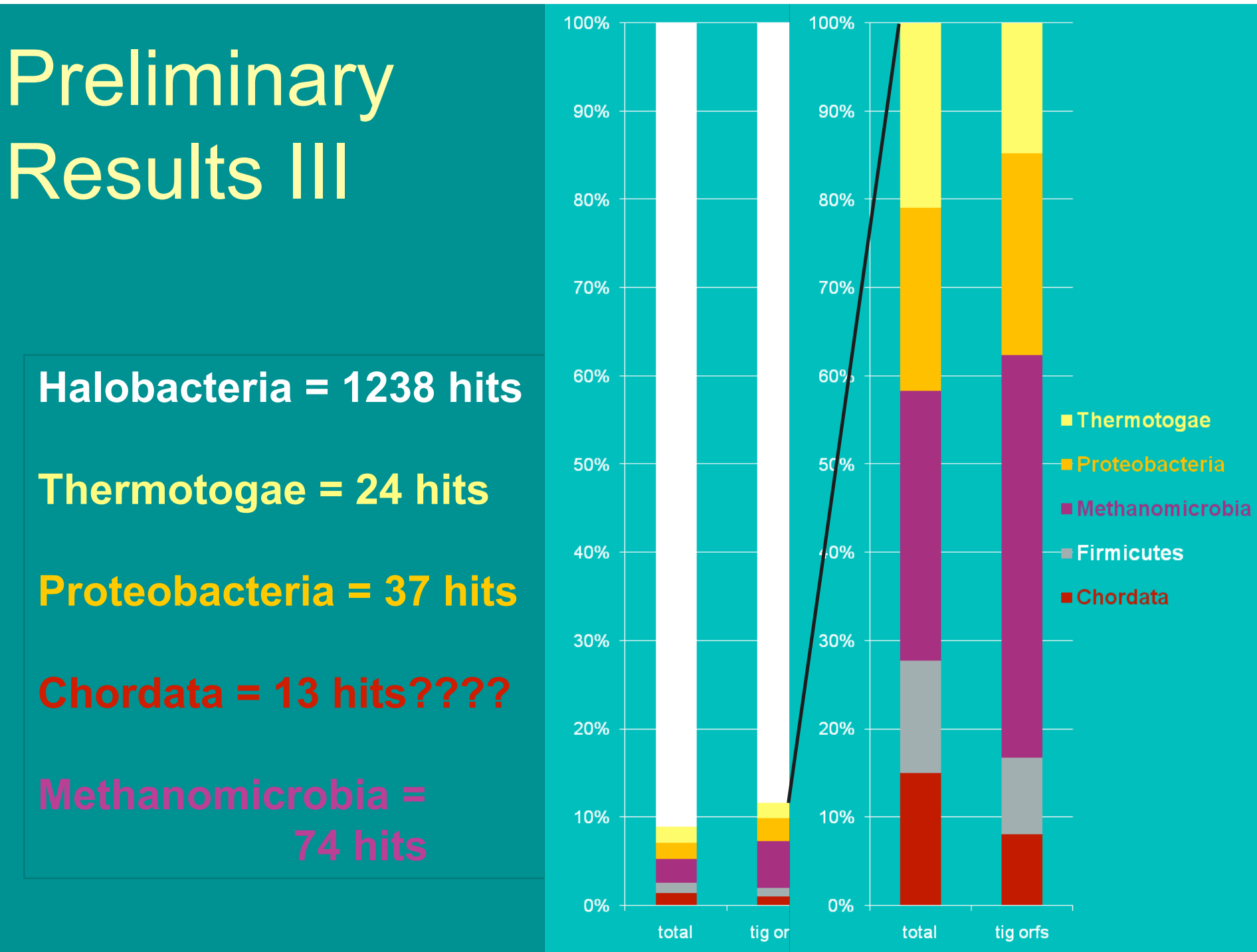
Number of other large fosmid contigs

3. Metagenomes sequenced:

½ plate 1992 after whole genome amplification

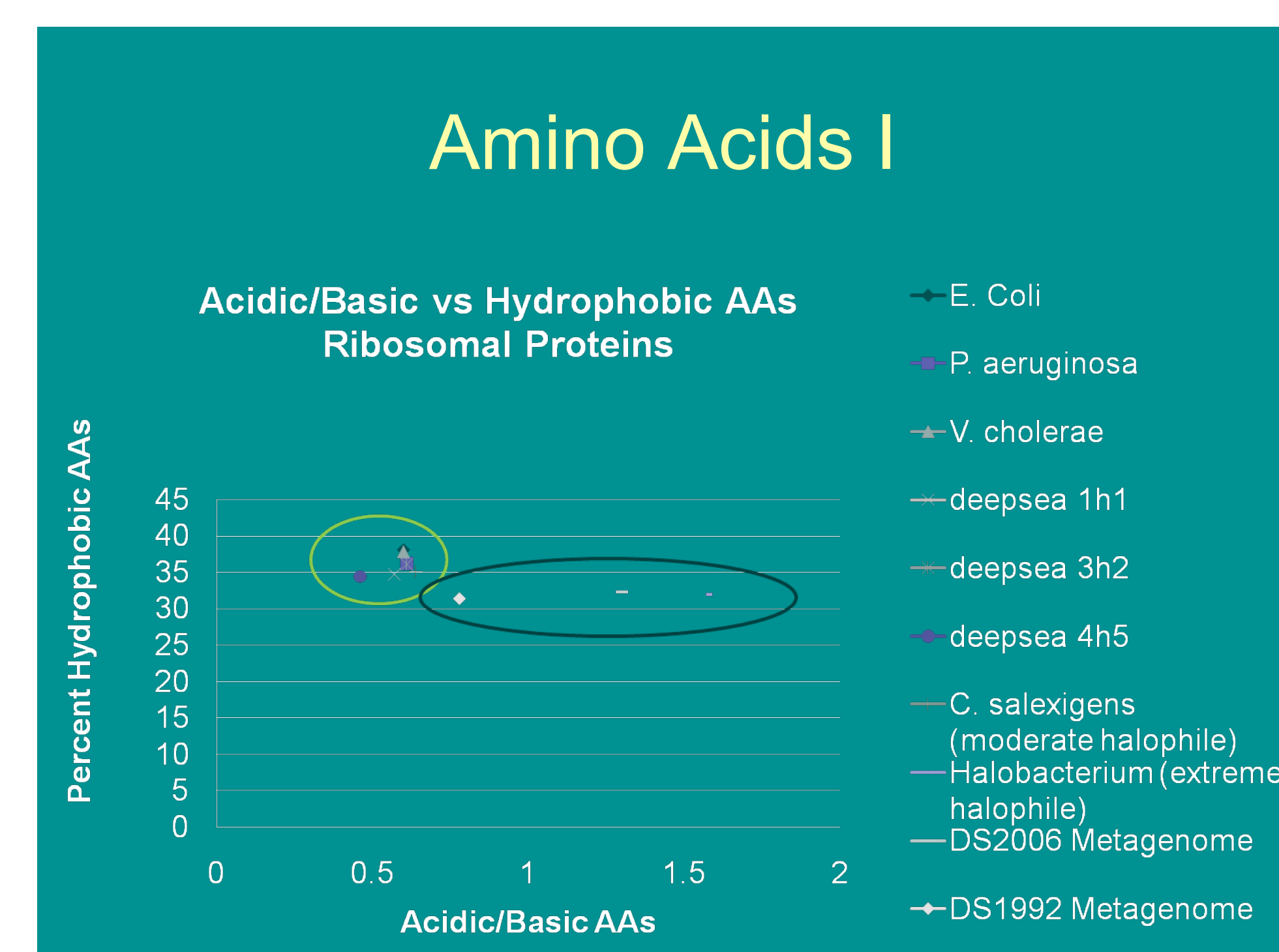
½ plate of modern Dead Sea

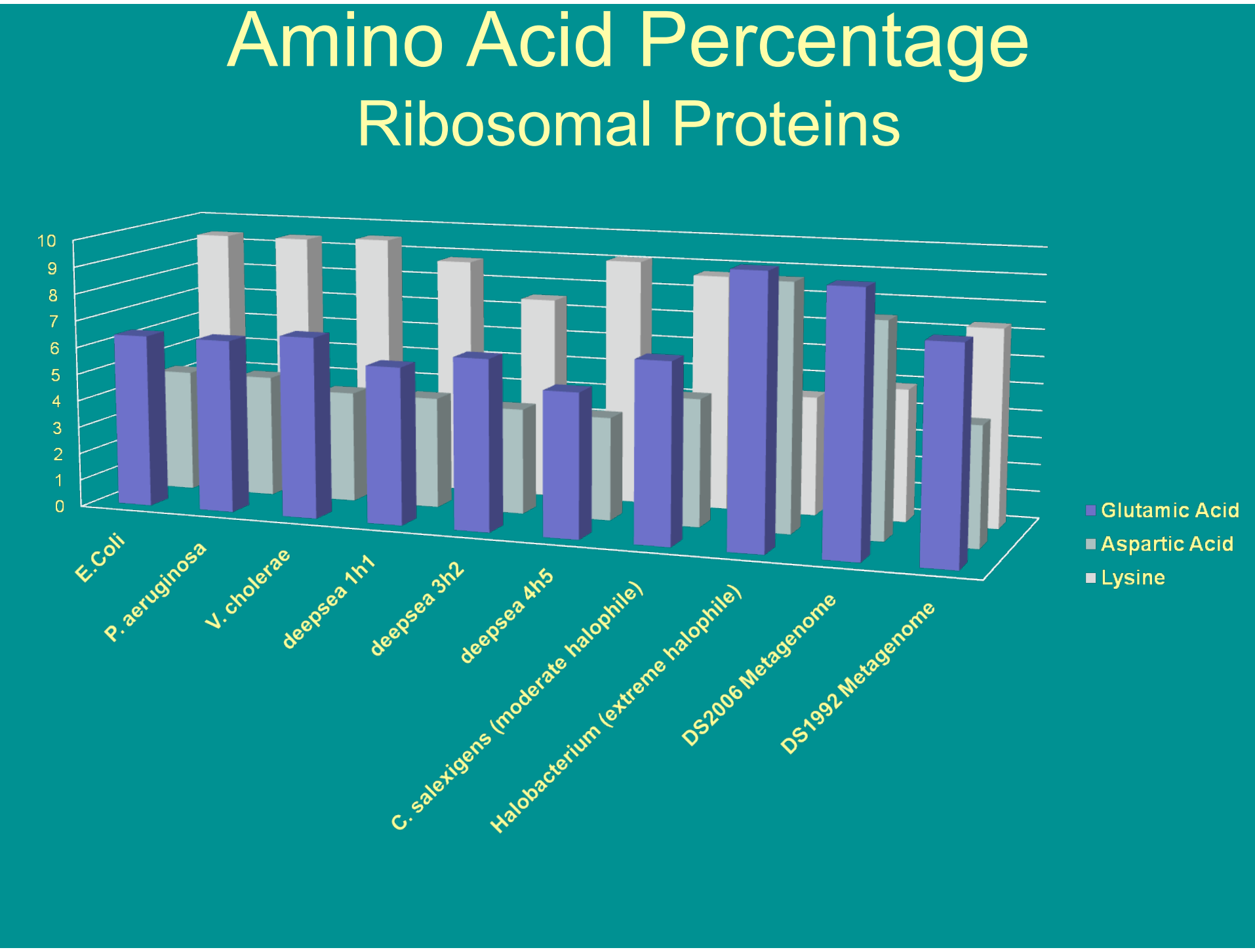


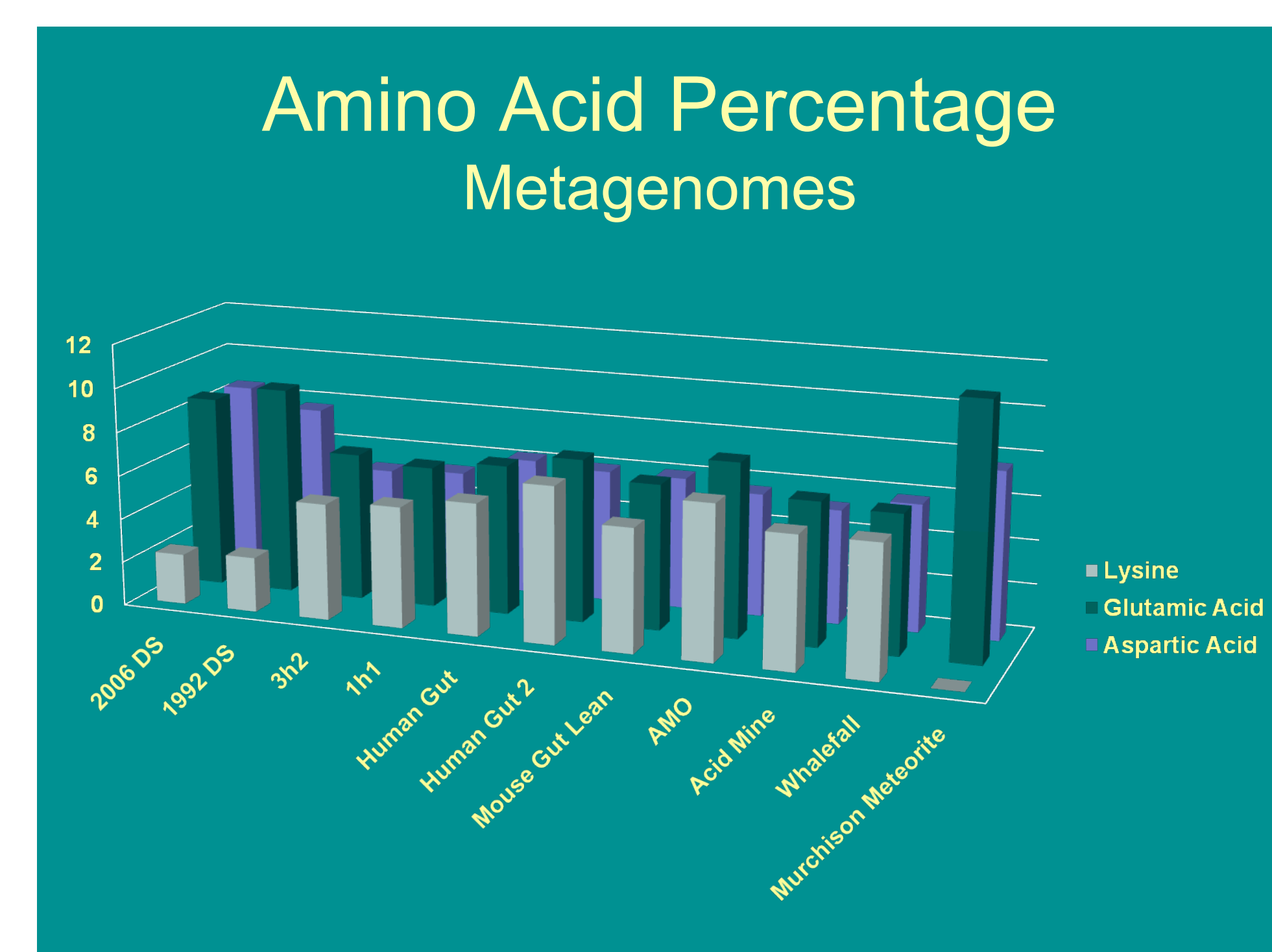


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## Summary

1. Identify a high number of DNA-based signatures of hypersaline life
2. Reveal organic biosignatures (cells, lipids, phospholipids, and amino acids) from the water and sediments
3. Integrate results with measured geochemistry
4. Involve international expert collaborators in analyzing the results

## Acknowledgments

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